

10 B.2

# Gap Results

**Refine**GAP of: 1169 seq 10 check: 1278 from: 1 to: 3792to: 1169 seq 2 check: 3043 from: 1 to: 1638Symbol comparison table: nwsgapdna.cmp CompCheck: 8760

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	0.000

Quality:	5384	Length:	3793
Ratio:	3.287	Gaps:	17

Percent Similarity: 40.134 Percent Identity: 40.134

Match display thresholds for the alignment(s):

| = IDENTITY

: = 5

. = 1

1169 seq 10 x 1169 seq 2 March 19, 2003 16:09 ..

```
901 tttcgcatgtatcagaatggcgaggttgccgacgttggcaaagtctttac 950
      ||||      |  || |      | || | |  |||
1  .....atgtcggccaccagcaactccagaggcgattgttccgtcgcatg 44
      .          .          .          .          .
951 tgttgtcctttccgtcaccttagcagccacgtccatctcaatgcttgccg 1000
      | | | |  |||      |  ||  |||||  |
45 cgacgccatcatcgttggagccggcctcagcggcatctctgctgtgtaca 94
      .          .          .          .          .
1001 cttcaggttcagtcgtttaccaacgccgcaccttcggctccgaattattc 1050
      |  |  ||  | |  |  |||||  |
95  aattgcgaaagctcagactcaacgccaaaatcttcgagggagccccgat 144
      .          .          .          .          .
1051 agtatcattgacaaaccacgcagctcgaccctctcgacccttctggaaa 1100
      |  |  | |  | |  | | | | ||||  ||  | |  ||
145 tttggcggcgtctggcactggaaccgctaccctggcgctcgtgttgattc 194
      .          .          .          .          .
1101 gcagccagagggctgcctaggtcaaattgagatccaaaacctggcatttg 1150
      | || |  || || |  | |||  |  | |
195 ggagacgcccttctaccaactgaacattcccgaagtatggaaagactgga 244
      .          .          .          .          .
1151 cctacccctcccgaccatctgccaagtacttcgagatttcaacttgaca 1200
      |||  | | |||  ||| |||  ||  |
245 cctggtcttgccgctatcctgacca.....gaaagagttg 279
      .          .          .          .          .
1201 attccagctggcaagacgacggccctcgtcgggtgcatcaggtagcggcaa 1250
      |  ||  ||  |  |  ||  || | |  | | | |
280 ctgtcatatgttcaccactgtgacaagatccggggcttgagaaaagacgt 329
      .          .          .          .          .
1251 aagcacaatggtcggcttacttgaacgggtgggtatctgccagttcgggga 1300
      |  |  |  |||  | ||||  | || |||  |||
```

```
330 ctacttcggagctgaggtgggtgatgcgcggtat.gccagagatctgggc 378
      . . . . .
1301 ggatattacttgatgggttggaactgggacaataacaatgtgaaatggctg 1350
      | | | | | | | | | |
379 acctggactgtcaagacgtcggctggccatgttgcgacggcaaagtatct 428
      . . . . .
1351 agaagccgcattcgcctcgttcaacaggaacctgtgttgtttcgtggcac 1400
      ||| | | | | | | | | |
429 cattctcgctacgggggttgctccacaggaagcacact.....cc 467
      . . . . .
1401 aatcttccagaacattgccaacgggtttcatggatgagcaacgagatctgc 1450
      ||| | | | | | | | |
468 cgcactccccggcctcgccgatttcaacgggaaggtgattcattcgagtg 517
      . . . . .
1451 ctcgcgaaaaacaaatggagcttgtgcaaaaagcttgcaaagccagcaat 1500
      | | | | | | | | | |
518 cctggcacgaagacttcgacgcagagggccagagagtcgccgtcatcggt 567
      . . . . .
1501 ggcgacgtgttcattaatgagcttccgaacggttatgagactgaagttgg 1550
      | | | | | | | | | |
568 gccggggccacaagcatccagattgttcaggagttggccaagaaggctga 617
      . . . . .
1551 cgagcgagccggagccttgagtggaggtcaacgacaacgaattgcaatcg 1600
      | | | | | | | | | |
618 ccaggtaacc.....atgtttatgcgaaggccgagctattgtctgcc 659
      . . . . .
1601 cacgaagtatcatatcggatcccaagatcctgttactcgatgaagctacc 1650
      | | | | | | | | | |
660 catgcggcaacgaa.....cgatggataggaacgaacagacagcctgg 702
      . . . . .
```

1651 agcgcccttgacccgaaggcggagaaagtgggtccaggaggccttgaaccg 1700  
| ||| |||| | | | ||| | | || | || |  
703 aaggcctactaccccacgctgtttgaagcgagtcgaaagtctcggattgg 752  
.  
1701 agtgtccaaagaccgcactactttgggtcattgccacaaactagccactg 1750  
| | | | || | | | || | || | | | |  
753 a...ttcccgggtccaggcacccgtcgggtggcatctttgaagtcagccccg 799  
.  
1751 tcaaaagtgctggcaacatcgcagtcattttcccaggggaaaatcgtcgag 1800  
| | | | | ||| || | | || | | | |  
800 agcagcgggaggcctatttcgaagagttgtgggagcgtggggcctttaat 849  
.  
1801 caaggcacacaccacgaattgatcgaattcgggtgtcattacgccgcact 1850  
| ||| | | || || || || | | | |  
850 tttcttgcttgcca.gtaccgagaagtcatgggttgacaaaaaggccaacc 898  
.  
1851 ggtgcgtgcacaggacctcggggctgacgaacaacaagaacatgagaaga 1900  
| || | || || | || || |  
899 gactgggtctatgacttctgggccaaaaagactcgatctcgtatcgtcaat 948  
.  
1901 ccctgcacgaaaaggcagcacgagaagctgctgggtgaacgaccggcactt 1950  
|| | || | | | ||| | | || || |  
949 ccggcaaagagagatctcatggctcctctggagccgcccgtactggttcgg 998  
.  
1951 gagcgactcacaccactgccacatctcaagctggaga.cctggagaagc 1999  
| | | | ||||| | | || | |||| ||||  
999 taccaagcgctccccactggagagcgactactacgaaatgctggacaagc 1048  
.  
2000 ggaaggtgccggtcgggactttgggctactcgctcctaaaatgcatccta 2049  
|| || | | || | | | |||| |

file://C:\WINNT\Temporary%20Internet%20Files\OLKE\seq%2010%20vs%202%20nucl... 3/20/2003

2400 actgtcagctctacccacgcagttgcaagagttgatatcagcaaattttc 2449

| | | | | | | | | | | | | | |

1392 ggaggccgagcacgccacgtccgttgaggcgacgaaatcagcaca.agag 1440

. . . . .

2450 tcatttatatcgttgtcgggtcaacatcgctctgagcagtgctctaccact 2499

| | | | | | | | | | | | | | |

1441 gcatggtcgattatgattgccaaagatgaacgagcacactctgttcccctt 1490

. . . . .

2500 agcctatggatggaaactgggcctgggtggttggtggtgcacttccac 2549

| | | | | | | | | | | | | | |

1491 gacggattcgtgg.....tggactggaggcaacatccctgggaaagcaac 1535

. . . . .

2550 ccctgcttttggctggctacctcagaattcgctctagagacgaagctagaa 2599

| | | | | | | | | | | | | | |

1536 acgtgctttaaccttcata.ggcgggattgctctctatgagcagatctgt 1584

. . . . .

2600 gccggaaactcggcaaactttgcagaaagtgctgggcttgcaagcgaagc 2649

| | | | | | | | | | | | | | |

1585 caagagaaggtggccaattgggatgggtttgatgtgctt.catgctccct 1633

. . . . .

2650 agttaccgcatccggaccgtctcatctttgactctcgaaggccatgttc 2699

| |

1634 gctaa..... 1638

.

.

.

**Input Sequence: 1169\_seq\_10**

```
!!NA_SEQUENCE 1.0

1169_seq_10 Length: 3792 March 19, 2003 16:05 Type: N
Check: 1278 ..

      1 atggcagatg aatcggagaa acctcgacca aaccaagatg
gcagtgagtc
```

[View Sequence](#)

## Input Sequence: 1169\_seq\_2

```
!!NA_SEQUENCE 1.0

1169_seq_2 Length: 1638 March 19, 2003 16:04 Type: N
Check: 3043 ..

      1 atgtcggcca ccagcaactc cagaggcgat tgttcggtcg
catgcgacgc
```

[View Sequence](#)





# Gap Results

[Refine](#)

GAP of: seq\_3 check: 4503 from: 1 to: 545

to: seq\_8 check: 1671 from: 1 to: 525

Symbol comparison table: blosum62.cmp CompCheck: 1102

BLOSUM62 amino acid substitution matrix.

Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid  
substitution matrices from protein blocks. Proc. Natl. Acad.  
Sci. USA 89: 10915-10919.

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248

Quality:	7	Length:	1044
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Ratio:	0.013	Gaps:	2
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Percent Similarity: 30.769 Percent Identity: 26.923

Match display thresholds for the alignment(s):

| = IDENTITY

: = 2

. = 1

seq\_3 x seq\_8

March 20, 2003 10:46 ..

```
1 .....MS 2

451 VNVLAVVFTSVTTVFFSFPLTVPTAASTMNYTSAIIGVALALGVLNWVVH 500

3 ATSNSRGDCSVACDAIIVGAGLS.GISAVYKLRKLRLNAKIFEGAPDFGG 51
| . .| . | :||| |
501 ARKHYQGP.HLELDGRVVGAEFQVGP..... 525
```

### Input Sequence: seq\_3

```
!!AA_SEQUENCE 1.0

seq_3 Length: 545 March 20, 2003 10:41 Type: P Check:
4503 ..

1 MSATSNSRGD CSVACDAIIV GAGLSGISAV YKLRKLRLNA
KIFEGAPDFG
```

[View Sequence](#)

**Input Sequence: seq\_8**

```
!!AA_SEQUENCE 1.0
seq_8 Length: 525 March 20, 2003 10:42 Type: P Check:
1671 ..

      1 MDSRPSGYGE KGGTRQTTKN TETAAAGGAS ESLNVPLEKK
QFGTITIVSL
```

[View Sequence](#)